

GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: August 9, 2003, 16:24:23 ; Search time 15.5429 Seconds
(without alignments)
98.997 Million cell updates/sec

Title: US-09-905-691-4
Perfect score: 16
Sequence: 1 ARAARRARRARRAE 16

Scoring table: OLIGO 60.0 , Gapext 60.0
Gapop 60.0 ,

Searched: 283308 seqs, 96168682 residues

Word size : 0

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : PIR-76:*
1: PIR1:*
2: PIR2:*
3: PIR3:*
4: PIR4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query Match	Score	Length	DB ID	Description
1	9	56.2	105	2 D86976	probable integrati
2	9	56.2	190	2 B70899	probable mihf prot
3	8	50.0	336	2 T50935	isomerase/decarbox
4	8	50.0	356	2 A21198	H-2 class I histoc
5	8	50.0	383	2 F83490	probable multidrug
6	8	50.0	710	2 AD3479	ATP-dependent heli
7	8	50.0	897	2 T02808	conserved hypothet
8	8	50.0	998	2 T35745	probable ATP-bind
9	7	43.8	69	2 AD2110	hypothetical prote
10	7	43.8	77	2 AH0925	hypothetical prote
11	7	43.8	110	2 T30752	hypothetical prote
12	7	43.8	144	2 H72702	hypothetical prote
13	7	43.8	157	2 D70777	hypothetical prote
14	7	43.8	159	2 C83305	hypothetical prote
15	7	43.8	174	2 D87638	transcription regu
16	7	43.8	252	2 AB3618	high-affinity bran
17	7	43.8	263	1 C39741	hypothetical 29K p
18	7	43.8	292	2 J80233	trypsin-I - scall
19	7	43.8	315	2 G67464	nitrogen regulatio
20	7	43.8	336	2 E84295	hypothetical prote
21	7	43.8	338	2 D95851	probable oxidoredu
22	7	43.8	358	2 F87364	Hyd family secret
23	7	43.8	376	2 T35868	probable dipeptida
24	7	43.8	408	2 A87649	hypothetical prote
25	7	43.8	409	1 S72892	probable hexosyltr
26	7	43.8	411	2 H82998	probable 3-hydroxy
27	7	43.8	428	2 H87214	probable glycosyl
28	7	43.8	438	2 T36953	conserved hypothet
29	7	43.8	444	2 S35783	glycoprotein gx -

30 7 43.8 474 1 BVERCE
31 7 43.8 480 1 A70744
32 7 43.8 501 2 A87474
33 7 43.8 511 2 B87258
34 7 43.8 525 2 A72586
35 7 43.8 568 2 B87495
36 7 43.8 603 1 QOBED1
37 7 43.8 604 2 S39885
38 7 43.8 704 2 T02558
39 7 43.8 742 1 TNEB1
40 7 43.8 777 2 A87309
41 7 43.8 899 2 C93339
42 7 43.8 913 1 VGEPS
43 7 43.8 1318 1 QOBED1
44 7 43.8 1360 2 T06699
45 7 43.8 1394 2 S60762

ALIGNMENTS

RESULT 1

D86976

Probable integration host factor [Imported] - Mycobacterium leprae

C:Species: Mycobacterium leprae

C:Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 20-Apr-2001

C:Accession: D86976

R: Cole, S.T.; Eiglmeier, K.; Parkhill, J.; James, K.D.; Thomson, N.R.; Wheeler, P.R.;
eam, M.A.; Rutherford, K.M.

Nature 409, 1007-1011, 2001

A: Authors: Rutter, S.; Seeger, K.; Simon, S.; Simmonds, M.; Skelton, J.; Squares, R.

A: Title: Massive gene decay in the leprosy bacillus.

A: Reference number: A86909; MUID: 21128732; PMID: 11234002

A: Accession: D86976

A: Status: Preliminary

A: Molecule type: DNA

A: Residues: 1-105 <STO>

A: Cross-references: GB:AL450380; NID:gl13092744; PIDN:CAC30048.1; GSPDB:GNO0147

C: Genetics:

A: Gene: mihf

Query Match 56.2%; Score 9; DB 2; Length 105;
Best Local Similarity 100.0%; Pred. No. 0.38;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 AAARRARAE 15

Db 19 AAARRARAE 27

RESULT 2

B70899

Probable mihf protein - Mycobacterium tuberculosis (strain H37RV)

C:Species: Mycobacterium tuberculosis

C:Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 20-Jun-2000

C:Accession: B70899

R: Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordc
Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyc
Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.

Nature 393, 537-544, 1998

A: Authors: Squares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.

A: Title: Deciphering the biology of Mycobacterium tuberculosis from the complete gen

A: Reference number: A70500; MUID: 98295987; PMID: 9634230

A: Accession: B70899

A: Status: Preliminary; nucleic acid sequence not shown; translation not shown

A: Molecule type: DNA

A: Residues: 1-190 <COL>

A: Cross-references: GB:Z80108; GB:AL123456; NID:g3256012; PIDN:CAB02193.1; PID:g1542

A: Experimental source: strain H37RV

C: Genetics:

A: Gene: mihf

C: Superfamily: Mycobacterium tuberculosis probable mihf protein

Query Match 56.2%; Score 9; DB 2; Length 190;
Best Local Similarity 100.0%; Pred. No. 0.61;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 7 AARARARAE 15
DB 104 AARARARAE 112

RESULT 3

T50935
isomerase/decarboxylase homolog DICH [imported] - Pseudomonas abietaniphila
C:Species: Pseudomonas abietaniphila
C>Date: 21-Jul-2000 #sequence_revision 21-Jul-2000 #text_change 21-Jul-2000
C:Accession: T50935
R:Martin, V.J.; Mohn, W.W.
J. Bacteriol. 181:2675-2682, 1999
A:Title: A novel aromatic-ring-hydroxylating dioxygenase from the diterpenoid-degrading
A:Reference number: Z5281; MUID:99235742; PMID:10217753
A:Status: preliminary
A:Accession: T50935
A:Molecule type: DNA
A:Residues: 1-336 <VAR>
A:Cross-references: EMBL:AF119621; PIDN:AAD21070.1
A:Experimental source: strain BKME-9; ATCC700689
C:Genetics:
A:Gene: dith

Query Match 50.0%; Score 8; DB 2; Length 336;
Best Local Similarity 100.0%; Pred. No. 6.3;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 7 AARARARA 14
DB 105 AARARARA 112

RESULT 4

A21198
H-2 class I histocompatibility antigen pH-2D-24 - mouse
C:Species: Mus musculus (house mouse)
C>Date: 27-Jul-1990 #sequence_revision 31-Jul-1992 #text_change 23-Jul-1999
C:Accession: A21198
R:Lalanne, J.L.; Cochet, M.; Kummer, A.M.; Gachelin, G.; Kourilsky, P.
Proc. Natl. Acad. Sci. U.S.A. 80:7561-7565, 1983
A:Title: Different exon-intron organization at the 5' part of a mouse class I gene is us
A:Reference number: A21198; MUID:84170268; PMID:6143316
A:Accession: A21198
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-356 <LAL>
A:Cross-references: GB:K01182; NID:g199544; PIDN:AAA39653.1; PID:g387468
A:Note: the authors translated the codon CCC for residue 288 as Ser
C:Superfamily: class I histocompatibility antigen; immunoglobulin homology
F:205-270/Domain: immunoglobulin homology <IMM>

Query Match 50.0%; Score 8; DB 2; Length 356;
Best Local Similarity 100.0%; Pred. No. 6.6;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 3 RAARARAR 10
DB 20 RAARARAR 27

RESULT 5

F83490
probable multidrug resistance efflux pump PA1237 [imported] - Pseudomonas aeruginosa (st
C:Species: Pseudomonas aeruginosa
C>Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000
C:Accession: F83490
R:Stover, C.K.; Pham, X.O.; Erwin, A.L.; Mizoguchi, S.D.; Warrenner, P.; Hickey, M.J.; B

adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.
; Lory, S.; Olson, M.V.
Nature 406: 959-964, 2000
A:Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic
A:Reference number: AB2950; MUID:20437337; PMID:10984043
A:Accession: F83490
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-383 <STO>
A:Cross-references: GB:AE004553; GB:AE004091; NID:g9947164; PIDN:AAG04626.1; GSPDB
A:Experimental source: strain PA01
C:Genetics:
A:Gene: PA1237
C:Superfamily: multidrug resistance protein A; lipoyl/biotin-binding homology

Query Match 50.0%; Score 8; DB 2; Length 383;
Best Local Similarity 100.0%; Pred. No. 7;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 5 ARAAARRA 12
DB 187 ARAAARRA 194

RESULT 6

AD3479
ATP-dependent helicase hrpB BME11818 [imported] - Brucella melitensis (strain 16M)
C:Species: Brucella melitensis
C>Date: 01-Feb-2002 #sequence_revision 01-Feb-2002 #text_change 14-Apr-2003
C:Accession: AD3479
R:DelVecchio, V.G.; Kaputrai, V.; Redkar, R.J.; Patra, G.; Mujer, C.; Los, T.; Ival
; Mazur, M.; Goldsman, E.; Selkov, E.; Elzer, P.H.; Hagius, S.; O'Callaghan, D.; I
Proc. Natl. Acad. Sci. U.S.A. 99:443-448, 2002
A:Title: The genome sequence of the facultative intracellular pathogen Brucella mel
A:Reference number: AD3522; PMID:11756688
A:Accession: AD3479
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-710 <KUR>
A:Cross-references: GB:AE008917; PIDN:AAL52999.1; PID:g17983853; GSPDB:GN00190
A:Experimental source: strain 16M
C:Genetics:
A:Gene: BME11818
A:Map position: 1
C:Superfamily: HrpB type ATP-dependent RNA helicase

Query Match 50.0%; Score 8; DB 2; Length 710;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 4 ARAAARR 11
DB 156 ARAAARR 163

RESULT 7

T02808
conserved hypothetical protein YPL199c, L2602.6 [imported] - Leishmania major (str
C:Species: Leishmania major
C>Date: 24-Mar-1999 #sequence_revision 24-Mar-1999 #text_change 19-May-2000
C:Accession: D81457; T02808
R:Myler, P.J.; Audlem, L.; deVos, T.; Hixson, G.; Kiser, P.; Lemley, C.; Magness,
Proc. Natl. Acad. Sci. U.S.A. 96:2902-2906, 1999
A:Title: Leishmania major Friedlin chromosome 1 has an unusual distribution of prot
A:Reference number: A81455; MUID:99178987; PMID:10077609
A:Accession: D81457
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-897 <PVL>
A:Cross-references: GB:AE001274; NID:g3264850; PIDN:AAC24631.1; PID:g2995584; GSPDB
A:Experimental source: strain MHOM/IL/81/Friedlin
C:Genetics:
A:Gene: L2602.6

A:Map position: 1

Query Match 50.0%; Score 8; DB 2; Length 897;
Best Local Similarity 100.0%; Pred. No. 14;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 AAARRARA 14
|||||
DB 326 AAARRARA 333

RESULT 8

T35745
probable ATP-binding RNA helicase - Streptomyces coelicolor
C:Species: Streptomyces coelicolor
C:Date: 05-Nov-1999 #sequence_revision 05-Nov-1999 #text_change 05-Nov-1999
R:Saunders, D.C.; Harris, D.; Bentley, S.D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.
submitted to the EMBL Data Library, August 1999
A:Reference number: 221588
A:Accession: T35745
A:Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: DNA
A:Residues: 1-998 <SAU>
A:Cross-references: EMBL:AL109732; PIDN:CAB52056.1; GSPDB:GN00070; SCOEDB:SC7H2.14
A:Experimental source: strain A3(2)
C:Genetics:
A:Gene: SCOEDB:SC7H2.14

Query Match 50.0%; Score 8; DB 2; Length 998;
Best Local Similarity 100.0%; Pred. No. 15;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 AAAAAARR 11
|||||
DB 70 AAAAAARR 77

RESULT 9

AD2110
hypothetical protein ael2435 [imported] - Nostoc sp. (strain PCC 7120)
C:Species: Nostoc sp. PCC 7120
A:Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120
C:Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Dec-2002
C:Accession: AD2110
R:Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguchi,
Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S.
DNA Res. 8, 205-213, 2001
A:Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Ana
A:Reference number: AB1807; MUID:21595285; PMID:11759840
A:Accession: AD2110
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-69 <KUR>
A:Cross-references: GB:BA000019; PIDN:BA074134.1; PID:gl7131527; GSPDB:GN00179
A:Experimental source: strain PCC 7120
C:Genetics:
A:Gene: asl2435

Query Match 43.8%; Score 7; DB 2; Length 69;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 AAARRAR 13
|||||
DB 54 AAARRAR 60

RESULT 10

AH0925
hypothetical protein STY3665 [imported] - Salmonella enterica subsp. enterica serovar Ty
C:Species: Salmonella enterica subsp. enterica serovar Typhi
A:Note: this species has also been called Salmonella typhi

C:Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 18-Nov-2002
C:Accession: AH0925

R:Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Church,
th, T.; Conerton, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Far
S.; Moule, S.; O'Gaora, P.

Nature 413, 848-852, 2001

A:Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens,
A:Title: Complete genome sequence of a multiple drug resistant Salmonella enterica s

A:Reference number: AB0502; MUID:21534947; PMID:11677608

A:Accession: AH0925

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-77 <PAR>

A:Cross-references: GB:AL513382; PIDN:CAD09426.1; PID:gl6504543; GSPDB:GN00176

C:Genetics:

A:Gene: STY3665

Query Match 43.8%; Score 7; DB 2; Length 77;
Best Local Similarity 100.0%; Pred. No. 13;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 RRARAEA 16
|||||
DB 30 RRARAEA 36

RESULT 11

T30752
hypothetical protein 150R - Molluscum contagiosum virus 1
N:Alternate names: MC150R
C:Species: Molluscum contagiosum virus 1
C:Date: 05-Nov-1999 #sequence_revision 05-Nov-1999 #text_change 21-Jul-2000
C:Accession: T30752
R:Senkevich, T.G.; Bugert, J.J.; Sisler, J.R.; Koonin, E.V.; Darai, G.; Moss, B.
Science 273, 813-816, 1996
A:Title: Genome sequence of a human tumorigenic poxvirus: Prediction of specific ho
A:Reference number: 220876; MUID:96325459; PMID:8670425
A:Accession: T30752
A:Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: DNA
A:Residues: 1-110 <SEN>
A:Cross-references: EMBL:U60315; NID:gl491943; PIDN:AAC55278.1; PID:gl492093
C:Genetics:
A:Note: MC150R
C:Superfamily: Molluscum contagiosum virus 1 hypothetical protein 150R

Query Match 43.8%; Score 7; DB 2; Length 110;
Best Local Similarity 100.0%; Pred. No. 17;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 AAARRAR 13
|||||
DB 91 AAARRAR 97

RESULT 12

H72702
hypothetical protein APE1039 - Aeropyrum pernix (strain K1)
C:Species: Aeropyrum pernix
C:Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 20-Aug-1999
C:Accession: H72702
R:Kawarabayashi, Y.; Hino, Y.; Horikawa, H.; Yamazaki, S.; Haikawa, Y.; Jin-no, K.;
awa, H.; Takamiya, M.; Masuda, S.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki,
DNA Res. 6, 83-101, 1999
A:Title: Complete genome sequence of an aerobic hyper-thermophilic Crenarchaeon, Ae
A:Reference number: A72450; MUID:99310339; PMID:10382966
A:Accession: H72702
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-144 <KAW>
A:Cross-references: DBJ:AF000060; NID:gs104188; PIDN:BA080024.1; PID:dl043810; PID
A:Experimental source: strain K1
C:Genetics:

A:Gene: APE1039

Query Match 43.8%; Score 7; DB 2; Length 144;
 Best Local Similarity 100.0%; Pred. No. 21;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ARAARA 7
 |||||
 Db 4 ARAARA 10

RESULT 13

D70777

Hypothetical protein RV2232 - Mycobacterium tuberculosis (strain H37RV)

C:Species: Mycobacterium tuberculosis

C>Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 22-Oct-1999

C:Accession: D70777

R:Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.

i Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S.

Rajandream, M.A.; Rogers, J.; Kutter, S.; Seeger, K.; Skelton, S.; Squares, S.

Nature 393, 537-544, 1998

A:Authors: Squares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.

A:Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome

A:Reference number: A70500; MUID:98295987; PMID:9634230

A:Accession: D70777

A>Status: preliminary; nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 1-157 <COL>

A:Cross-references: GB:270692; GB:AL123456; NID:g3261567; PIDN:CAA94666.1; PID:el299960;

A:Experimental source: strain H37RV

C:Genetics:

A:Gene: RV2232

Query Match

43.8%; Score 7; DB 2; Length 157;

Best Local Similarity 100.0%; Pred. No. 23;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 ARAARA 12
 |||||
 Db 66 ARAARA 72

RESULT 14

C83305

Hypothetical protein PA2721 [Imported] - Pseudomonas aeruginosa (strain PA01)

C:Species: Pseudomonas aeruginosa

C>Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000

C:Accession: C83305

R:Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warren, P.; Hickey, M.J.; Br

adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim,

J.; Lory, S.; Olson, M.V.

Nature 406, 959-964, 2000

A:Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic path

A:Reference number: A82950; MUID:20437337; PMID:10984043

A:Accession: C83305

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-159 <STO>

A:Cross-references: GB:AE004700; GB:AE004091; NID:g9948792; PIDN:AAG06109.1; GSPDB:GN001

A:Experimental source: strain PA01

C:Genetics:

A:Gene: PA2721

Query Match

43.8%; Score 7; DB 2; Length 159;

Best Local Similarity 100.0%; Pred. No. 23;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 ARAARA 12
 |||||
 Db 132 ARAARA 138

RESULT 15

D87638

transcription regulator, GntR family [Imported] - Caulobacter crescentus

C:Species: Caulobacter crescentus

C>Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 20-Apr-2001

C:Accession: D87638

R:Nierman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg

B.; Laub, M.T.; DeBoy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.;

n, J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser,

Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001

A:Title: Complete Genome Sequence of Caulobacter crescentus.

A:Reference number: A87249; MUID:21173698; PMID:11259647

A:Accession: D87638

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-174 <STO>

A:Cross-references: GB:AE005673; NID:g13424808; PIDN:AAK25104.1; GSPDB:GN00148

C:Genetics:

A:Gene: CC3142

Query Match

43.8%; Score 7; DB 2; Length 174;

Best Local Similarity 100.0%; Pred. No. 25;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 ARAAAR 10
 |||||
 Db 50 ARAAAR 56

Search completed: August 9, 2003, 16:34:12

Job time : 16.5429 secs